

Claims

1. (Amended) A method for transforming a useful plant by introducing a gene of another species into the useful plant, wherein the gene of another species to be introduced does not contain sequence with continued 8 bases or more consisting of only G or T, and is designed not to contain any of base sequences represented by a sequence NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN, (wherein N in the base sequence is any one of bases), in the downstream of GT-rich base sequence in the base sequence of the gene of the other species without substantially altering the function of the protein encoded by the gene to be introduced.
2. The method according to claim 1, wherein the gene of another species to be introduced is derived from yeast.
3. (Cancelled)
4. (Cancelled)
5. (Amended) The method according to claim 1 or 2, wherein the modification of base sequence in the region of a factor relating to the poly (A) addition of the mRNA is performed based on a codon usage of the useful higher plant to be transformed.
6. The method according to any one of claims 1-5, wherein the modification of base sequence is performed for reducing base G and T rich region.
7. (Amended) The method according to any one of claims 1-6, wherein the difference between base G and base C covering throughout the region of gene is small to be introduced.
8. The method according to any one of claims 1-7, wherein the modification of base sequence is performed for not to have ATTTA sequence.
9. The method according to any one of claims 1-8, wherein the sequence located

at the upstream of the initiation codon of the gene to be introduced has Kozak sequence.

10. The method according to any one of claims 1-9, wherein the gene to be introduced encodes a protein involved in absorption of nutrition.

11. The method according to claim 10, wherein the gene to be introduced is the gene encoding ferric-chelate reductase FRE1.